



1600

## RAW SEQUENCE LISTING

DATE: 05/07/2003

PATENT APPLICATION: US/09/880,821A

TIME: 12:18:06

Input Set : A:\EP.txt

Output Set: N:\CRF4\05072003\I880821A.raw

5 <110> APPLICANT: EAGLES, Peter Anthony Minter  
 7 ZHENG, Richard Qihao  
 9 BTG INTERNATIONAL LIMITED  
 13 <120> TITLE OF INVENTION: RIBOZYMAL NUCLEIC ACID  
 17 <130> FILE REFERENCE: PF 137 765 WO/RKP  
 C--> 21 <140> CURRENT APPLICATION NUMBER: US/09/880,821A  
 C--> 23 <141> CURRENT FILING DATE: 2001-06-15  
 27 <150> PRIOR APPLICATION NUMBER: GB 9800870.9  
 29 <151> PRIOR FILING DATE: 1998-01-15  
 33 <150> PRIOR APPLICATION NUMBER: GB 9824794.3  
 35 <151> PRIOR FILING DATE: 1998-12-23  
 39 <160> NUMBER OF SEQ ID NOS: 15  
 43 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

323 <210> SEQ ID NO: 14  
 325 <211> LENGTH: 93 92 shown  
 327 <212> TYPE: DNA  
 329 <213> ORGANISM: Artificial Sequence  
 333 <220> FEATURE:  
 W--> 335 <223> OTHER INFORMATION:  
 W--> 335 <400>14  
 E--> 336 gggcgaaagc ccuagauugc ugaugagcgc gaaagcgcg aacuguccu cuacgaaagu  
 E--> 338 agagcugaug aaccgaaag gucgaaacaa gug  
 341 <210> SEQ ID NO: 15  
 343 <211> LENGTH: 100  
 345 <212> TYPE: DNA  
 347 <213> ORGANISM: Artificial Sequence  
 351 <220> FEATURE:  
 W--> 353 <223> OTHER INFORMATION:  
 W--> 353 <400>15  
 E--> 354 gggccgaaag gcccucacu cugaugagcg cgaaagcgcg aaacguuguc cucugagaaa  
 356 ucagagcuga ugagguccga aaggaccgaa acaacguuuc

pp 1-4  
 Does Not Comply  
 Corrected Diskette Needed

Per 1.822  
 of sequence  
 rules,  
 insert cumulative  
 base total at right  
 60 ← margin  
 92 93 of each  
 line

→ group of 9 (one missing)

see p.4

60 ← insert  
 100

see pp 2-3 for more errors

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2

<210> 1

<211> 13

<212> RNA

*invalid <213> response*

<213> CD4-positive T cell, CCR5 receptor

*see item 10 on Ena  
summary  
sheet*

<400> 1

*↓*

The sequence shown exist throughout  
the sequence. Please check subsequent  
sequences for errors.

&lt;210&gt; 13

&lt;211&gt; 48

&lt;212&gt; DNA

*see p. 4*<213> Artificial Sequence

&lt;220&gt;

&lt;400&gt;13

gggcgaaagc cucagauugc ugaugagcgc gaaagcggca aacuuguc

48

48 (see item 1  
on Enr summary  
sheet)

4

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/880,821A

DATE: 05/07/2003  
TIME: 12:18:07

Input Set : A:\EP.txt  
Output Set: N:\CRF4\05072003\I880821A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3,5,7,9,11,13,15,17,19,21,23,25,27,29,31,33,35,37,39,41,43  
Seq#:1; Line(s) 45,47,49,51,53,55,57,59,61,63  
Seq#:2; Line(s) 65,67,69,71,73,75,77,79  
Seq#:3; Line(s) 81,83,85,87,89,91,93,95  
Seq#:4; Line(s) 97,99,101,103,105,107,109,111  
Seq#:5; Line(s) 113,115,117,119,121,123,125,127,129,131,133,135,137,139,141  
Seq#:6; Line(s) 143,145,147,149,151,153,155,157,159  
Seq#:7; Line(s) 161,163,165,167,169,171,173,175,177  
Seq#:8; Line(s) 179,181,183,185,187,189,191,193,195,197,199,201,203,205,207  
Seq#:9; Line(s) 209,211,213,215,217,219,221,223,225,227,229,231  
Seq#:10; Line(s) 233,235,237,239,241,243,245,247,249,251,253,255  
Seq#:11; Line(s) 257,259,261,263,265,267,269,271,273,275,277,279,281  
Seq#:12; Line(s) 283,285,287,289,291,293,295,297,299,301,303,305,307,308  
Seq#:13; Line(s) 310,312,314,316,318,321,323  
Seq#:14; Line(s) 325,327,329,331,333,338,341  
Seq#:15; Line(s) 343,345,347,349,351

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:13,14,15

*error explanation*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/880,821A

DATE: 05/07/2003

TIME: 12:18:07

Input Set : A:\EP.txt

Output Set: N:\CRF4\05072003\I880821A.raw

L:21 M:270 C: Current Application Number differs, Replaced Application Number  
L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:320 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>  
ORGANISM:Artificial Sequence  
L:320 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:320  
L:335 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>  
ORGANISM:Artificial Sequence  
L:335 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:335  
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14  
M:254 Repeated in SeqNo=14  
L:338 M:252 E: No. of Seq. differs, <211> LENGTH:Input:93 Found:92 SEQ:14  
L:353 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>  
ORGANISM:Artificial Sequence  
L:353 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:353  
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15

# **NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

## **Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

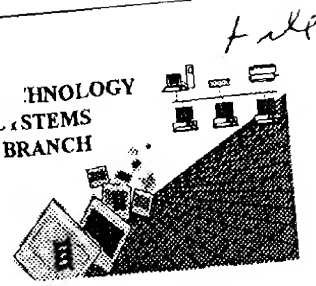
## SUGGESTED CORRECTION

SERIAL NUMBER:

09/880,821A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



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TEL: 202-757-1600/2900

form: \_\_\_\_\_

Application Serial Number: 09/880,821A

Source: 1690

Date Processed by STIC: 5/7/2003

SELECTED ERRORS.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:  
<http://www.uspto.gov/web/offices/pac/checker>

TRADEMARK OFFICE

<http://www.uspto.gov/web/offices/pac/checkcr>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

[http://www.uspto.gov/patents/submitting/sequence/sequence-downloads/documents.htm](#), EFS Submission

- Any reply including a sequence listing in electronic form must be filed with the United States Patent and Trademark Office, and instead should be sent via <http://www.uspto.gov/efc/efc/downloads/documents.htm>, EFS Submission
1. EFS-Bio (<<http://www.uspto.gov/efc/efc/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
  2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
  3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
  4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003